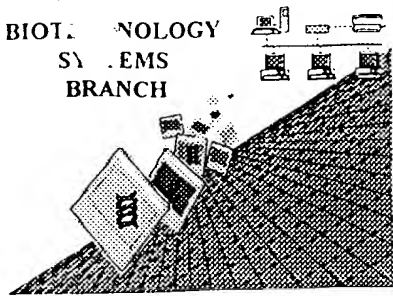


5. Letters

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/430,590 C #14
Source: 1636
Date Processed by STIC: 3-9-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable-form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/430,590C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☒ Variable Length
Sequence(s) ^{1,2} contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)
Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/430,590C

DATE: 03/09/2001
TIME: 11:58:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\03092001\I430590C.raw

**Does Not Comply
Corrected Diskette Needed**

see pp. 1,5

3 <110> APPLICANT: Poulter, et al.
5 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPONSON FROM THE YEAST CANDIDA ALBICANS
7 <130> FILE REFERENCE: 674521-2001.1
9 <140> CURRENT APPLICATION NUMBER: 09/430,590C
10 <141> CURRENT FILING DATE: 1999-10-29
12 <150> PRIOR APPLICATION NUMBER: 60/106,342
13 <151> PRIOR FILING DATE: 1998-10-30
15 <160> NUMBER OF SEQ ID NOS: 156
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 13
21 <212> TYPE: DNA
22 <213> ORGANISM: Candida albicans
24 <220> FEATURE:
25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (7)..(7)
27 <223> OTHER INFORMATION: nucleotide 'n' represents the 376 nucleotide sequence in between
28 the inverted repeats of the LTR of TCa1 in Candida albican
31 <300> PUBLICATION INFORMATION:
32 <308> DATABASE ACCESSION NO: AF043301
33 <309> DATABASE ENTRY DATE: 1998-07-21
34 <313> RELEVANT RESIDUES: (1)..(13)
36 <400> SEQUENCE: 1

W--> 37 **tgttcgncga aca**

13

40 <210> SEQ ID NO: 2
41 <211> LENGTH: 19
42 <212> TYPE: DNA
43 <213> ORGANISM: Candida albicans
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature,
47 <222> LOCATION: (10)..(10)
48 <223> OTHER INFORMATION: nucleotide 'n' represents the 382 nucleotide sequence in between
49 the inverted repeats of the LTR of another element in Candida alb
50 ican
53 <300> PUBLICATION INFORMATION:
54 <308> DATABASE ACCESSION NO: Y08494
55 <309> DATABASE ENTRY DATE: 1997-08-27
56 <313> RELEVANT RESIDUES: (1)..(19)
58 <400> SEQUENCE: 2

W--> 59 **taatgtatan tatacaaca**

19

62 <210> SEQ ID NO: 3
63 <211> LENGTH: 6426
64 <212> TYPE: DNA
65 <213> ORGANISM: Candida albicans
67 <220> FEATURE:
68 <221> NAME/KEY: CDS
69 <222> LOCATION: (398)..(1372)

*Variable length error.
"n" may only represent
a single residue. See
#6 on the Error Summary
Sheet.*

*Variable length error
see above.*

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MAR 22 2001

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/430,590C

DATE: 03/09/2001
TIME: 11:58:25

Input Set : A:\ES.txt

Output Set: N:\CRF3\03092001\I430590C.raw

```

70 <223> OTHER INFORMATION: ORF1 coding sequence for gag
73 <220> FEATURE:
74 <221> NAME/KEY: CDS
75 <222> LOCATION: (1373)..(6103)
76 <223> OTHER INFORMATION: ORF2 - coding sequence for pol
79 <400> SEQUENCE: 3
80 tgttggtttg tgcactatatt tgtgtcagaa actgatcaat gaaaatgatg gttattatga      60
82 gaatggaaaa tttttccatc acacatcagg tgaatgacaga actaaactat attgtgtagt      120
84 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt      180
86 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt      240
88 acacgctcaa tctcaggtaa agaaagttaa tattccatca gattagaagt cgatagtgat      300
90 aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt      360
92 gatagtttcg aagtttgaag gtacagaatt tcacaagatg agt tcc gca aag aat      415
93                                     Met Ser Ser Ala Lys Asn
94                                     1           5
96 gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct      463
97 Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala
98      10           15           20
100 att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc      511
101 Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe
102      25           30           35
104 ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc      559
105 Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser
106      40           45           50
108 gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc      607
109 Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro
110 55           60           65           70
112 gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag      655
113 Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys
114      75           80           85
116 gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg      703
117 Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met
118      90           95           100
120 tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tct aag      751
121 Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys
122      105           110           115
124 cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat      799
125 Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr
126      120           125           130
128 gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg      847
129 Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu
130 135           140           145           150
132 ctg aag ttt gta aac gtt gaa cat gag tta gtg gtt tgc tat aac ctt      895
133 Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu
134      155           160           165
136 cca tat ttg ctg cag gtg gaa gag aaa ctt gag gaa ata ctc tac aac      943
137 Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn
138      170           175           180
140 act tca aac gtt gtc gat gag tat gtc cgt agt ctt cca aat ctc ata      991

```

RAW SEQUENCE LISTING
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Input Set : A:\ES.txt
 Output Set: N:\CRF3\03092001\I430590C.raw

141	Thr	Ser	Asn	Val	Val	Asp	Glu	Tyr	Val	Arg	Ser	Leu	Pro	Asn	Leu	Ile	
142			185						190				195				
144	ggt	caa	gtc	ttg	tac	ttc	aat	cat	gtg	aag	aaa	tca	gag	gct	tta	agt	1039
145	Gly	Gln	Val	Leu	Tyr	Phe	Asn	His	Val	Lys	Lys	Ser	Glu	Ala	Leu	Ser	
146		200					205					210					
148	ttg	ttt	ttg	aat	att	cat	gcc	tca	tac	tac	tca	aag	tggt	att	caa	gct	1087
149	Leu	Phe	Leu	Asn	Ile	His	Ala	Ser	Tyr	Tyr	Ser	Lys	Trp	Ile	Gln	Ala	
150	215					220					225				230		
152	gac	aat	gat	aca	tca	gta	ctc	cca	agt	tgct	tct	acc	ata	gct	gaa	gaa	1135
153	Asp	Asn	Asp	Thr	Ser	Val	Leu	Pro	Ser	Cys	Ser	Thr	Ile	Ala	Glu	Glu	
154				235						240				245			
156	atg	tgt	gat	cat	cct	gat	tat	gct	aga	ttg	ggt	gac	att	cca	agc	aac	1183
157	Met	Cys	Asp	His	Pro	Asp	Tyr	Ala	Arg	Leu	Val	Asp	Ile	Pro	Ser	Asn	
158			250						255				260				
160	aaa	tat	gaa	ctt	aat	ctt	att	gtt	agt	tta	cca	gca	cca	gag	aaa	cca	1231
161	Lys	Tyr	Glu	Leu	Asn	Leu	Ile	Val	Ser	Leu	Pro	Ala	Pro	Glu	Lys	Pro	
162		265					270					275					
164	aaa	gga	aaa	cca	gag	gag	aac	tca	ctg	gaa	caa	tct	caa	aag	aag	aac	1279
165	Lys	Gly	Lys	Pro	Glu	Glu	Asn	Ser	Ser	Glu	Gln	Ser	Gln	Lys	Lys	Asn	
166		280					285					290					
168	ctg	aaa	tca	aga	aag	aga	aat	aag	aaa	cat	cca	aaa	tca	gat	aac	gat	1327
169	Ser	Lys	Ser	Arg	Lys	Arg	Asn	Lys	Lys	His	Pro	Lys	Ser	Asp	Asn	Asp	
170	295				300					305				310			
172	aaa	ggt	gaa	aaa	gaa	aaa	gaa	aaa	gaa	aaa	act	tca	ctg	gaa	tga	aaa	1375
173	Lys	Gly	Glu	Lys	Glu	Lys	Glu	Lys	Glu	Lys	Thr	Ser	Ser	Glu		Lys	
174				315						320					325		
176	aca	ggt	gct	gct	tct	att	aat	tgt	gta	atg	aat	ata	cat	aat	tgc	agc	1423
177	Thr	Gly	Ala	Ala	Ser	Ile	Asn	Cys	Val	Met	Asn	Ile	His	Asn	Cys	Ser	
178				330						335				340			
180	aaa	acc	acg	ttt	cca	gta	gaa	aat	tct	cat	tct	ctt	aat	gct	tct	ttg	1471
181	Lys	Thr	Thr	Phe	Pro	Val	Glu	Asn	Ser	His	Ser	Leu	Asn	Ala	Ser	Leu	
182			345						350				355				
184	aac	gta	atg	aat	ttt	aaa	ggt	tta	agg	ttt	aac	aag	tat	cta	gtg	tat	1519
185	Asn	Val	Met	Asn	Phe	Lys	Gly	Leu	Arg	Phe	Asn	Lys	Tyr	Leu	Val	Tyr	
186		360					365					370					
188	gat	act	ggt	gcc	aca	ata	tct	gtt	gtg	aac	aat	aaa	gat	ata	ttg	ctg	1567
189	Asp	Thr	Gly	Ala	Thr	Ile	Ser	Val	Val	Asn	Asn	Lys	Asp	Ile	Leu	Ser	
190		375				380					385						
192	aat	gtt	aag	gac	gca	aca	att	gaa	gtt	tct	gtt	gct	gat	ggt	gct	aca	1615
193	Asn	Val	Lys	Asp	Ala	Thr	Ile	Glu	Val	Ser	Val	Ala	Asp	Gly	Ala	Thr	
194	390				395					400				405			
196	tta	gaa	gca	gat	tgt	att	ggt	gat	cta	att	atc	aga	gtc	ggt	att	gtc	1663
197	Leu	Glu	Ala	Asp	Cys	Ile	Gly	Asp	Leu	Ile	Ile	Arg	Val	Gly	Ile	Val	
198				410					415				420				
200	tcg	att	acg	tta	gag	aat	aca	ttg	tat	tta	cca	gaa	agt	tcc	ttt	aat	1711
201	Ser	Ile	Thr	Leu	Glu	Asn	Thr	Leu	Tyr	Leu	Pro	Glu	Ser	Ser	Phe	Asn	
202			425						430				435				
204	ctt	gtg	agt	ttg	aaa	caa	att	gaa	gaa	cga	gga	ttt	aat	gtt	ctt	att	1759
205	Leu	Val	Ser	Leu	Lys	Gln	Ile	Glu	Glu	Arg	Gly	Phe	Asn	Val	Leu	Ile	

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206	440	445	450	
208	act aaa gaa tca gtg att gta ttt aac caa aat gtg gct cct act att	1807		
209	Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr Ile			
210	455 460 465			
212	att gct tca agg aag aat gct gct gat ctt tat atg ggt cct caa ttc	1855		
213	Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln Phe			
214	470 475 480 485			
216	agt gaa gaa tct tta gaa tgt gat ttt gat tat gat ggt ttg gca gat	1903		
217	Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala Asp			
218	490 495 500			
220	atg ttg tcc aat gct aac caa gat gac aaa gat aaa tca agt atg aat	1951		
221	Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met Asn			
222	505 510 515			
224	gaa atg tca gaa tat caa gaa cat gat tat agt tct cga gca tta ata	1999		
225	Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu Ile			
226	520 525 530			
228	aat tct ttg acg gag gtt gat gtt tta gat gtt gaa att tcc cca tat	2047		
229	Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro Tyr			
230	535 540 545			
232	gga gtt gaa caa ttg cta cca act gga gat aag aac gat att tat aat	2095		
233	Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr Asn			
234	550 555 560 565			
236	ttc cat ttg atg tca aat cat atg tcc att gag aaa atc ttg ttg tta	2143		
237	Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu Leu			
238	570 575 580			
240	caa aaa tac cag ggt ctc gta ctt cac act tca aaa gag agt ctt caa	2191		
241	Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu Gln			
242	585 590 595			
244	aag att gct gat tgt aag gta tgt cta tta tcg aat gcc aaa cag aga	2239		
245	Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln Arg			
246	600 605 610			
248	agt cac aat cat cat tca gaa aga aaa gcc tcg aga aga cat gag aga	2287		
249	Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu Arg			
250	615 620 625			
252	ctt cat tgt gat act ctc ggt cca ttt agg tcc gaa aat aac aag tgg	2335		
253	Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys Trp			
254	630 635 640 645			
256	tat tta acg tct gtt ata gat gaa cat acg ggt tac att gaa gga att	2383		
257	Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly Ile			
258	650 655 660			
260	att act aaa gac aga aag gta aag gat ctc tta att caa cga tta aag	2431		
261	Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu Lys			
262	665 670 675			
264	atc tgg aat aat cgg ttt aac gat aag gtg gca tac ttc aga agt gat	2479		
265	Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser Asp			
266	680 685 690			
268	aat gct cct gag ttc cca caa cct tct gat tta gct gag ttc ggt att	2527		
269	Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly Ile			
270	695 700 705			

RAW SEQUENCE LISTING

DATE: 03/09/2001

PATENT APPLICATION: US/09/430,590C

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Input Set : A:\ES.txt

Output Set: N:\CRF3\03092001\I430590C.raw

272	tgg	agg	gag	act	ata	gcg	gca	tat	ctg	cct	gag	ctt	aat	ggt	ctc	gcc	2575
273	Trp	Arg	Glu	Thr	Ile	Ala	Ala	Tyr	Ser	Pro	Glu	Leu	Asn	Gly	Leu	Ala	
274	710					715					720					725	
276	gag	gtt	gtt	aat	aaa	ttg	att	tta	caa	cag	att	tac	agg	atc	gtt	gtg	2623
277	Glu	Val	Val	Asn	Lys	Leu	Ile	Leu	Gln	Gln	Ile	Tyr	Arg	Ile	Val	Val	
278					730					735					740		
280	aca	ctt	ggt	cca	caa	ata	ctc	aag	ttg	att	tat	tat	gtg	att	caa	tat	2671
281	Thr	Leu	Gly	Pro	Gln	Ile	Leu	Lys	Leu	Ile	Tyr	Tyr	Val	Ile	Gln	Tyr	
282					745					750					755		
284	tct	att	aca	atg	atc	aac	cac	act	cca	cgt	cgt	tca	ctc	aag	gga	caa	2719
285	Ser	Ile	Thr	Met	Ile	Asn	His	Thr	Pro	Arg	Arg	Ser	Leu	Lys	Gly	Gln	
286				760					765					770			
288	acc	cct	tat	ggt	tgc	tat	tat	caa	tta	agt	gag	gga	aat	ttc	tac	cgg	2767
289	Thr	Pro	Tyr	Gly	Cys	Tyr	Tyr	Gln	Leu	Ser	Glu	Gly	Asn	Phe	Tyr	Arg	
290				775				780					785				
292	ttt	cct	ttt	gcc	atc	gat	tgt	gtc	gtt	aca	ttt	agt	aat	gcc	atc	gaa	2815
293	Phe	Pro	Phe	Ala	Ile	Asp	Cys	Val	Val	Thr	Phe	Ser	Asn	Ala	Ile	Glu	
294	790					795					800					805	
296	aag	aac	cgt	tac	gga	gtt	aca	tca	act	aaa	gga	gct	cct	tca	tcg	atc	2863
297	Lys	Asn	Arg	Tyr	Gly	Val	Thr	Ser	Thr	Lys	Gly	Ala	Pro	Ser	Ser	Ile	
298					810					815					820		
300	atg	ggt	gct	gtg	att	ggc	tac	gct	agc	gat	tgt	ttt	agt	tat	tac	gtg	2911
301	Met	Gly	Ala	Val	Ile	Gly	Tyr	Ala	Ser	Asp	Cys	Phe	Ser	Tyr	Tyr	Val	
302					825					830					835		
304	ttg	cta	aaa	aat	atg	cgg	tgt	gat	att	atc	ctt	agc	cct	aat	gtc	cgt	2959
305	Leu	Leu	Lys	Asn	Met	Arg	Cys	Asp	Ile	Ile	Leu	Ser	Pro	Asn	Val	Arg	
306				840				845						850			
308	ata	ttg	cga	agc	tat	gag	gtt	att	aac	tcc	tat	ctc	aaa	aac	tta	tcc	3007
309	Ile	Leu	Arg	Ser	Tyr	Glu	Val	Ile	Asn	Ser	Tyr	Leu	Lys	Asn	Leu	Ser	
310				855				860						865			
312	act	aca	cct	atg	tca	cac	att	gtt	cct	atg	gct	gaa	ggt	atc	cag	gga	3055
313	Thr	Thr	Pro	Met	Ser	His	Ile	Val	Pro	Met	Ala	Glu	Gly	Ile	Gln	Gly	
314	870					875					880					885	
316	agg	caa	ctg	ggc	gct	cag	tac	gag	gta	cgc	gga	aca	tat	gtg	gaa	agt	3103
317	Arg	Gln	Ser	Gly	Ala	Gln	Tyr	Glu	Val	Arg	Gly	Thr	Tyr	Val	Glu	Ser	
318					890					895					900		
320	gaa	tat	gac	aat	aca	aat	gac	gtg	atg	cac	atg	ccc	aaa	gag	tca	tat	3151
321	Glu	Tyr	Asp	Asn	Thr	Asn	Asp	Val	Met	His	Met	Pro	Lys	Glu	Ser	Tyr	
322				905						910					915		
324	tca	gtt	cag	cca	gca	tcg	ttt	act	tta	act	acg	ggt	aac	agt	tct	aac	3199
325	Ser	Val	Gln	Pro	Ala	Ser	Phe	Thr	Leu	Thr	Thr	Gly	Asn	Ser	Ser	Asn	
326				920						925					930		
328	gaa	tat	gtt	ata	aat	gat	gat	cca	gta	cag	att	acc	att	gag	aat	ccc	3247
329	Glu	Tyr	Val	Ile	Asn	Asp	Asp	Pro	Val	Gln	Ile	Thr	Ile	Glu	Asn	Pro	
330				935				940				945					
332	gat	gat	ttt	tct	aac	cct	ctt	caa	cta	act	gaa	gaa	tca	cac	gat	atg	3295
333	Asp	Asp	Phe	Ser	Asn	Pro	Leu	Gln	Leu	Thr	Glu	Glu	Ser	His	Asp	Met	
334	950					955						960				965	
336	gta	tcc	gaa	gta	aaa	tcg	gat	gag	aat	cct	aaa	ccc	agt	ctc	cac	gag	3343

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 03/09/2001

PATENT APPLICATION: US/09/430,590C

TIME: 11:58:26

Input Set : A:\ES.txt

Output Set: N:\CRF3\03092001\I430590C.raw

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:2246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:2266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:2356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:2496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:3147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:3271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:3429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:3493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:3543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:3625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:3645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:3647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:3759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:3821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:3877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:3993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33

VERIFICATION SUMMARY

DATE: 03/09/2001

PATENT APPLICATION: US/09/430,590C

TIME: 11:58:26

Input Set : A:\ES.txt

Output Set: N:\CRF3\03092001\I430590C.raw

L:3995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33

L:5079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85